

University of Nebraska - Lincoln

DigitalCommons@University of Nebraska - Lincoln

---

US Army Research

U.S. Department of Defense

---

2013

# Bacterial Peritonitis Due to *Acinetobacter baumannii* Sequence Type 25 with Plasmid-Borne New Delhi Metallo-Beta-Lactamase in Honduras

Paige E. Waterman

*Walter Reed Army Institute of Research*

Patrick McGann

*Walter Reed Army Institute of Research*

Erik Snesrud

*Walter Reed Army Institute of Research*

Robert J. Clifford

*Walter Reed Army Institute of Research*

Yoon I. Kwak

*Walter Reed Army Institute of Research*

*See next page for additional authors*

Follow this and additional works at: <http://digitalcommons.unl.edu/usarmyresearch>

---

Waterman, Paige E.; McGann, Patrick; Snesrud, Erik; Clifford, Robert J.; Kwak, Yoon I.; Munoz-Urbizo, Ivon P.; Tabora-Castellanos, Juana; Milillo, Michael; Preston, Lan; Aviles, Ricardo; Sutter, Deena E.; and Lesho, Emil P., "Bacterial Peritonitis Due to *Acinetobacter baumannii* Sequence Type 25 with Plasmid-Borne New Delhi Metallo-Beta-Lactamase in Honduras" (2013). *US Army Research*. 298. <http://digitalcommons.unl.edu/usarmyresearch/298>

This Article is brought to you for free and open access by the U.S. Department of Defense at DigitalCommons@University of Nebraska - Lincoln. It has been accepted for inclusion in US Army Research by an authorized administrator of DigitalCommons@University of Nebraska - Lincoln.

---

**Authors**

Paige E. Waterman, Patrick McGann, Erik Snesrud, Robert J. Clifford, Yoon I. Kwak, Ivon P. Munoz-Urbizo, Juana Tabora-Castellanos, Michael Milillo, Lan Preston, Ricardo Aviles, Deena E. Sutter, and Emil P. Lesho

# Bacterial Peritonitis Due to *Acinetobacter baumannii* Sequence Type 25 with Plasmid-Borne New Delhi Metallo- $\beta$ -Lactamase in Honduras

Paige E. Waterman,<sup>a</sup> Patrick McGann,<sup>a</sup> Erik Snestrud,<sup>a</sup> Robert J. Clifford,<sup>a</sup> Yoon I. Kwak,<sup>a</sup> Ivón P. Munoz-Urbizo,<sup>b</sup> Juana Tabora-Castellanos,<sup>b</sup> Michael Milillo,<sup>a</sup> Lan Preston,<sup>a</sup> Ricardo Aviles,<sup>c</sup> Deena E. Sutter,<sup>d</sup> Emil P. Lesho<sup>a</sup>

Multidrug-resistant Organism Repository and Surveillance Network, Walter Reed Army Institute of Research, Silver Spring, Maryland, USA<sup>a</sup>; Department of Epidemiology, Hospital Escuela, Tegucigalpa, Honduras<sup>b</sup>; Medical Element, Joint Task Force-Bravo, Soto Cano Air Base, Honduras<sup>c</sup>; Division of Pediatric Infectious Disease, San Antonio Military Medical Center, Fort Sam Houston, Texas, USA<sup>d</sup>

**A carbapenem-resistant *Acinetobacter baumannii* strain was isolated from the peritoneal fluid of a patient with complicated intra-abdominal infection and evaluated at the Multidrug-resistant Organism Repository and Surveillance Network by whole-genome sequencing and real-time PCR. The isolate was sequence type 25 and susceptible to colistin and minocycline, with low MICs of tigecycline. *bla*<sub>NDM-1</sub> was located on a plasmid with >99% homology to pNDM-BJ02. The isolate carried numerous other antibiotic resistance genes, including the 16S methylase gene, *armA*.**

Carbapenem-resistant Gram-negative organisms are emerging pathogens that threaten global public health and seriously challenge infection control and therapy efforts (1–3). Though still relatively uncommon, the carbapenemase encoded by *bla*<sub>NDM</sub> has quickly established itself as one of the most important (4). First described in 2009 (5), the gene has since been identified in nearly every continent and has been detected in species as diverse as *Acinetobacter baumannii* and *Vibrio cholerae* (6–8). Furthermore, the gene has been associated with a diverse range of plasmids that often harbor multiple antibiotic resistance genes (9).

In 2012, the Multidrug-resistant Organism Repository and Surveillance Network (MRSN) (10) received a request from a Ministry of Health hospital in Tegucigalpa, Honduras, for assistance in identifying the genetic mechanism associated with an extensively drug-resistant (XDR) isolate of *A. baumannii*. The isolate was recovered from a 76-year-old male patient admitted for ongoing dialysis in the setting of dysfunctional hemodialysis access. On the second day of admission, a peritoneal catheter was placed and the patient was prescribed empirical ciprofloxacin (250 mg) and a single dose of cephalothin (2 g). Two days later, the patient developed a fever (38.2°C) and experienced right lower abdominal pain. Peritoneal fluid cultures revealed moderate growth of Gram-negative bacilli. The patient was prescribed ceftriaxone (2 g/day) followed by intravenous ciprofloxacin (200 mg every 12 h) and intraperitoneal ceftazidime (250 mg). The organism was identified as *A. baumannii* with resistance to the fluoroquinolones and  $\beta$ -lactams, including carbapenems. Prompt clinical improvement followed removal of the peritoneal dialysis catheter and the initiation of tigecycline (50 mg every 12 h). He was discharged 17 days later and completed a 10-day course of therapy with tigecycline.

The isolate was forwarded to the MRSN and tested for carbapenemase genes by real-time PCR (11). Identification and antibiotic susceptibility tests were performed on three automated systems: the Vitek 2 (bioMérieux, Inc., NC), the BD Phoenix (BD Diagnostics Systems, MD), and the Microscan Walk-Away (Siemens Healthcare Diagnostics Inc., IL). MICs of colistin, minocycline, polymyxin B, and tigecycline were determined by Etest; colistin susceptibility was also assayed using broth microdilution.

Whole genome sequencing was performed using an Ion Torrent Personal Genome Machine (PGM) with 200-bp chemistry.

The isolate (MRSN 12227) was identified as *A. baumannii*. It was resistant to amikacin, ampicillin-sulbactam, aztreonam, cefepime, cefotaxime, ceftazidime, ceftriaxone, ciprofloxacin, gentamicin, imipenem, levofloxacin, meropenem, tetracycline, tobramycin, and trimethoprim-sulfamethoxazole using CLSI breakpoints (12). The isolate was susceptible to minocycline (MIC = 3  $\mu$ g/ml) and to colistin by broth microdilution (MIC = 0.25  $\mu$ g/ml) and Etest (MIC = 0.125  $\mu$ g/ml). It had low MICs of tigecycline (1.5  $\mu$ g/ml) and polymyxin B (0.25  $\mu$ g/ml), which correlate with the successful treatment of the patient with tigecycline.

MRSN 12227 was assigned to sequence type 25 (ST25) (Pasteur scheme), an ST that has been sporadically identified in a number of countries, including The Netherlands, Turkey, Greece, Italy, Sweden, and Singapore, and is not associated with any clonal complex (13, 14). Though sporadic, ST25 appears to be a stable clone and has been implicated in clinical infections since 1985 (14).

Mean coverage depth for genome assembly was 129-fold. MRSN 12227 carried *bla*<sub>NDM-1</sub> on a plasmid that shared >99% homology to pNDM-BJ02, a plasmid initially identified in a clinical isolate of *Acinetobacter lwoffii* in Beijing, China (15). Interestingly, we also identified this plasmid in a clinical isolate of *A. schindleri* recovered from a surveillance groin swab of a U.S. service member wounded in Afghanistan (16). This plasmid is unclassifiable by PCR-based replicon typing, has a novel plasmid backbone sequence, and carries genes that encode a type IV secretion system (T4SS) that facilitates horizontal transmission (15). The composition of the genetic region surrounding *bla*<sub>NDM</sub> shares

Received 7 February 2013 Returned for modification 8 April 2013

Accepted 26 June 2013

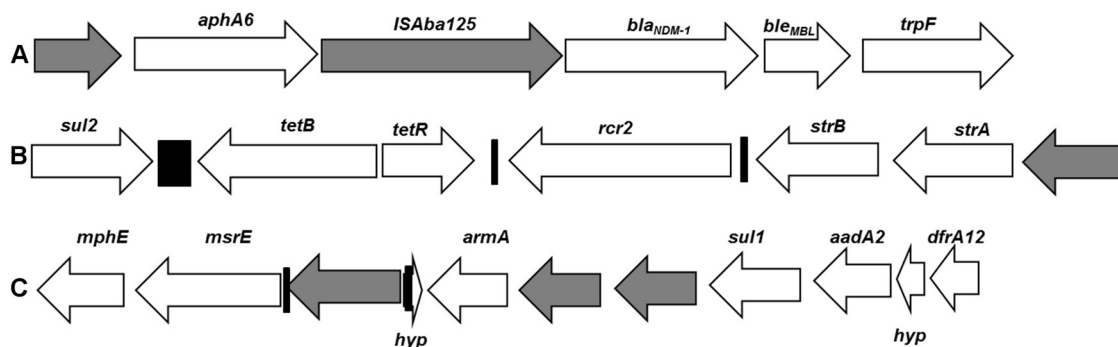
Published ahead of print 1 July 2013

Address correspondence to Paige E. Waterman, paige.e.waterman.mil@mail.mil, or Patrick McGann, patrick.t.mcgann4.ctr@mail.mil.

P.E.W. and P.M. contributed equally to this article.

Copyright © 2013, American Society for Microbiology. All Rights Reserved.

doi:10.1128/AAC.00275-13



**FIG 1** Composition of the genetic environment surrounding *bla*<sub>NDM-1</sub> (A), the *AbaR* resistance island (B), and the 16S methylase gene *armA* (C). Arrows indicate gene orientation from 5' to 3'. Relative gene sizes are proportional to the lengths of the arrows. White arrows indicate confirmed or putative functional genes with hypothetical genes, marked as *hyp*. Gray arrows indicate transposons, and black bars indicate repeat regions.

common elements with other plasmids carrying *bla*<sub>NDM</sub> in *Enterobacteriaceae* (17), including the putative bleomycin resistance gene *ble*<sub>MDL</sub>, the *N*-(5'-phosphoribosyl)anthranilate isomerase gene *trpF*, and the insertion sequence *ISAbA125* (Fig. 1). pNDM-BJ02 also carries a nonfunctional copy of *aphA6*, which normally encodes an aminoglycoside-modifying enzyme (AME) that confers resistance to amikacin. The same genetic architecture is apparent in the plasmid from MRSN 12227, with an upstream transposition event seemingly disrupting the promoter region of *aphA6*. However, unlike the *A. lwoffii* (15) and *A. schindleri* (16) isolates that also carried this plasmid, MRSN 12227 is resistant to amikacin. This discrepancy was resolved when further analysis of the MRSN 12227 genome using ResFinder (18) revealed a chromosomal copy of the 16S methylase gene, *armA*, which confers

resistance to all aminoglycosides (19) (Table 1). pNDM-BJ02 has been reported to have a very high frequency of transfer ( $9.1 \times 10^{-3}$  to  $1.3 \times 10^{-2}$  per donor cell) to *Escherichia coli* J53 Azi<sup>r</sup> (15). Our experience with *bla*<sub>NDM</sub>-carrying strains of *Acinetobacter* provides further evidence for the promiscuity of this plasmid. In both instances in which the MRSN has encountered *bla*<sub>NDM</sub>-carrying strains of *Acinetobacter*, pNDM-BJ02 has been its vehicle of transmission.

MRSN 12227 also carries plasmid pCTXM360, which harbors the  $\beta$ -lactamase gene *bla*<sub>CTX-M-15</sub> (20), and has two additional chromosomal insertions carrying multiple antibiotic resistance genes (Table 1 and Fig. 1). The first of these carries six antibiotic resistance loci, including the aforementioned 16S methylase gene *armA* and the macrolide resistance genes *mphE* and *msrE* (Table 1

**TABLE 1** Antibiotic resistance genes carried by MRSN 12227<sup>a</sup>

Gene <sup>b</sup>	Contig <sup>c</sup>	Location <sup>d</sup>	Function <sup>e</sup>	Notes
<i>bla</i> <sub>OXA-64</sub>	1	Chromosome	Class D $\beta$ -lactamase	<i>bla</i> <sub>OXA-51</sub> -like
<i>mphE</i>	1	Chromosome	Macrolide phosphotransferase	Confers resistance to macrolides
<i>msrE</i>	1	Chromosome	Macrolide efflux protein	Confers resistance to macrolides
<i>armA</i>	1	Chromosome	16S methylase	Confers resistance to all aminoglycosides
<i>sul1</i>	1	Chromosome	Dihydropteroate synthase	Confers resistance to sulfonamides
<i>ant(3'')-Ia</i>	1	Chromosome	AME	<i>aadA2</i> ; confers resistance to gentamicin and tobramycin
<i>dfrA-12</i>	1	Chromosome	Dihydrofolate reductase	Confers resistance to trimethoprim
<i>ceoA</i> -like	6	Chromosome	RND efflux pump	98% identity to <i>CeoB</i> (protein) <sup>f</sup>
<i>ceoB</i>	6	Chromosome	RND efflux pump	
<i>opcM</i> -like	6	Chromosome	RND efflux pump	
<i>sul2</i>	38	Chromosome	Dihydropteroate synthase	Confers resistance to sulfonamides
<i>tetB</i>	38	Chromosome	Efflux pump	Confers resistance to tetracycline
<i>aph(6)-Id</i>	38	Chromosome	AME	<i>strB</i> ; confers resistance to streptomycin
<i>aph(3'')-Ib</i>	38	Chromosome	AME	<i>strA</i> ; confers resistance to streptomycin
<i>bla</i> <sub>CTX-M-15</sub>	44	pCTXM360	ESBL	Confers resistance to cephalosporins and monobactams
<i>aph(3')-VIa</i>	50	pNDM-BJ02	AME	Nonfunctional
<i>bla</i> <sub>NDM-1</sub>	50	pNDM-BJ02	Class B $\beta$ -lactamase	Confers resistance to all $\beta$ -lactams except aztreonam
<i>aac(3)-IIa</i>	56	Putative Plasmid	AME	Confers resistance to gentamicin and tobramycin
<i>bla</i> <sub>TEM-1</sub>	59	Unknown	ESBL	3 synonymous SNPs <sup>g</sup> ; resistance to early cephalosporins

<sup>a</sup> Abbreviations: AME, aminoglycoside-modifying enzyme; ESBL, extended-spectrum  $\beta$ -lactamases; SNP, single-nucleotide polymorphism; RND, resistance/nodulation/division.

<sup>b</sup> Based on closest match to BLAST (<http://blast.ncbi.nlm.nih.gov>) search.

<sup>c</sup> The MRSN 12227 whole-genome sequence was assembled into 95 contigs. The relative sizes of the reported contigs (in base pairs) are as follows: contig 1, 383,184; contig 6, 197,316; contig 38, 23,159; contig 44, 13,686; contig 50, 8,127; contig 56, 1,720; and contig 59, 1,375.

<sup>d</sup> Putative or confirmed location of the respective antibiotic resistance gene based on whole-genome sequencing.

<sup>e</sup> Confirmed or putative function of protein.

<sup>f</sup> Confers resistances to chloramphenicol, trimethoprim, and ciprofloxacin.

<sup>g</sup> *bla*<sub>TEM-1</sub> contains 3 synonymous mutations compared to the reference *bla*<sub>TEM-1</sub> sequence (26). pCTXM-360 contains *bla*<sub>TEM</sub> in close proximity to *bla*<sub>CTX-M-15</sub>, but the exact location of *bla*<sub>TEM-1</sub> is still uncertain.

and Fig. 1). This structure has been identified on plasmids associated with *Klebsiella oxytoca* and *Citrobacter freundii* (GenBank accession numbers CP003684.1 and JX182975.1, respectively) and on the chromosome of *A. baumannii* MDR-TJ and TYTH-1 (21, 22). The second region also includes multiple antibiotic resistance genes, including the tetracycline efflux gene *tetB*, the streptomycin resistance genes *strA* and *strB*, and the dihydropteroate synthase gene *sul2*. This region most closely resembles the *Acinetobacter* resistance island AbaR1 (23), which is widely distributed in *Acinetobacter baumannii* strains. MRSN 12227 carries the chromosomally encoded *bla*<sub>OXA-51</sub>-like gene *bla*<sub>OXA-64</sub> but does not carry any acquired class D carbapenemase genes, indicating that carbapenemase resistance in this strain is probably due to *bla*<sub>NDM-1</sub>.

This is the first report of *bla*<sub>NDM</sub> from Honduras, and it follows the recent identification of this gene in a strain of *Klebsiella pneumoniae* in neighboring Guatemala (24). The current epidemiological evidence from the hospital supports nosocomial transmission of MRSN 12227, but further investigations are ongoing. The modified Hodge test and the Carba NP tests were both negative for MRSN 12227, but this is not unexpected for *Acinetobacter* (25). Finally, pNDM-BJ02 appears to be emerging as a common vehicle for the horizontal transmission of *bla*<sub>NDM</sub>, particularly in *Acinetobacter* species. *In vitro* evidence suggests that this plasmid is highly promiscuous, and further research is warranted to see if this plasmid is capable of being transmitted and stably maintained in other clinically important bacteria.

## ACKNOWLEDGMENTS

Major funding for this study was provided by the U.S. Army Medical Command (MEDCOM) and the Department of Defense Global Emerging Infections Surveillance and Response System (GEIS). We gratefully acknowledge the support of Guy Lemire and Bart Diaz at the Joint Task Force-Bravo, Soto Cano Air Base, Honduras. We also gratefully acknowledge the support and assistance of Douglas Lougee, a surgeon with the U.S. Southern Command (USSOUTHCOM). We thank Blanca Hernández and Fanny Hidalgo, Facultad de Microbiología, Universidad Nacional Autónoma de Honduras, for isolate collection and transport.

Material has been reviewed by the Walter Reed Army Institute of Research. There is no objection to its presentation. The opinions or assertions contained herein are the private views of the authors and are not to be construed as official, or reflecting the views of the Department of the Army or the Department of Defense.

## REFERENCES

- Livermore DM. 2012. Current epidemiology and growing resistance of gram-negative pathogens. *Korean J. Intern. Med.* 27:128–142.
- Nordmann P, Dortet L, Poirel L. 2012. Carbapenem resistance in *Enterobacteriaceae*: here is the storm! *Trends Mol. Med.* 18:263–272.
- Patel G, Bonomo RA. 2011. Status report on carbapenemases: challenges and prospects. *Expert Rev. Anti Infect. Ther.* 9:555–570.
- Nordmann P, Poirel L, Walsh TR, Livermore DM. 2011. The emerging NDM carbapenemases. *Trends Microbiol.* 19:588–595.
- Yong D, Toleman MA, Giske CG, Cho HS, Sundman K, Lee K, Walsh TR. 2009. Characterization of a new metallo-beta-lactamase gene, *bla*(NDM-1), and a novel erythromycin esterase gene carried on a unique genetic structure in *Klebsiella pneumoniae* sequence type 14 from India. *Antimicrob. Agents Chemother.* 53:5046–5054.
- Bushnell G, Mitrani-Gold F, Mundy LM. 15 January 2013, posting date. Emergence of New Delhi metallo-beta-lactamase type 1-producing *Enterobacteriaceae* and non-*Enterobacteriaceae*: global case detection and bacterial surveillance. *Int. J. Infect. Dis.* [Epub ahead of print.] doi:10.1016/j.ijid.2012.11.025.
- Darley E, Weeks J, Jones L, Daniels V, Wootton M, MacGowan A, Walsh T. 2012. NDM-1 polymicrobial infections including *Vibrio cholerae*. *Lancet* 380:1358.
- Karthikeyan K, Thirunarayan MA, Krishnan P. 2010. Coexistence of *bla*<sub>OXA-23</sub> with *bla*<sub>NDM-1</sub> and *armA* in clinical isolates of *Acinetobacter baumannii* from India. *J. Antimicrob. Chemother.* 65:2253–2254.
- Walsh TR, Weeks J, Livermore DM, Toleman MA. 2011. Dissemination of NDM-1 positive bacteria in the New Delhi environment and its implications for human health: an environmental point prevalence study. *Lancet Infect. Dis.* 11:355–362.
- Waterman P, Kwak Y, Clifford R, Julius M, Onmus-Leone F, Tsurgeon C, Riley M, Black C, McGann P, Lesho E. 2012. A multidrug-resistance surveillance network: 1 year on. *Lancet Infect. Dis.* 12:587–588.
- Milillo M, Kwak YI, Snesrud E, Waterman PE, Lesho E, McGann P. 2013. Rapid and simultaneous detection of *bla*<sub>KPC</sub> and *bla*<sub>NDM</sub> by use of multiplex real-time PCR. *J. Clin. Microbiol.* 51:1247–1249.
- Clinical and Laboratory Standards Institute. 2011. Performance standards for antimicrobial susceptibility testing: 19th informational supplement. CLSI document M100-S21. Clinical and Laboratory Standards Institute, Wayne, PA.
- Di Popolo A, Giannouli M, Triassi M, Brisse S, Zarrilli R. 2011. Molecular epidemiological investigation of multidrug-resistant *Acinetobacter baumannii* strains in four Mediterranean countries with a multilocus sequence typing scheme. *Clin. Microbiol. Infect.* 17:197–201.
- Karah N, Sundsfjord A, Townner K, Samuelsen O. 2012. Insights into the global molecular epidemiology of carbapenem non-susceptible clones of *Acinetobacter baumannii*. *Drug Resist. Updat.* 15:237–247.
- Hu H, Hu Y, Pan Y, Liang H, Wang H, Wang X, Hao Q, Yang X, Yang X, Xiao X, Luan C, Yang Y, Cui Y, Yang R, Gao GF, Song Y, Zhu B. 2012. Novel plasmid and its variant harboring both a *bla*(NDM-1) gene and type IV secretion system in clinical isolates of *Acinetobacter lwoffii*. *Antimicrob. Agents Chemother.* 56:1698–1702.
- McGann P, Milillo M, Clifford RJ, Snesrud E, Stevenson L, Backlund MG, Viscount HB, Quintero R, Kwak YI, Zapor MJ, Waterman PE, Lesho EP. 3 April 2013, posting date. Detection of New Delhi metallo-beta-lactamase (*bla*<sub>NDM-1</sub>) in *Acinetobacter schindleri* during routine surveillance. *J. Clin. Microbiol.* [Epub ahead of print.] doi:10.1128/JCM.00281-13.
- Poirel L, Dortet L, Bernabeu S, Nordmann P. 2011. Genetic features of *bla*<sub>NDM-1</sub>-positive *Enterobacteriaceae*. *Antimicrob. Agents Chemother.* 55:5403–5407.
- Zankari E, Hasman H, Kaas RS, Seyfarth AM, Agerso Y, Lund O, Larsen MV, Aarestrup FM. 2013. Genotyping using whole-genome sequencing is a realistic alternative to surveillance based on phenotypic antimicrobial susceptibility testing. *J. Antimicrob. Chemother.* 68:771–777.
- Galimand M, Courvalin P, Lambert T. 2003. Plasmid-mediated high-level resistance to aminoglycosides in *Enterobacteriaceae* due to 16S rRNA methylation. *Antimicrob. Agents Chemother.* 47:2565–2571.
- Zhu WH, Luo L, Wang JY, Zhuang XH, Zhong L, Liao K, Zeng Y, Lu YJ. 2009. Complete nucleotide sequence of pCTX-M360, an intermediate plasmid between pEL60 and pCTX-M3, from a multidrug-resistant *Klebsiella pneumoniae* strain isolated in China. *Antimicrob. Agents Chemother.* 53:5291–5293.
- Huang H, Yang ZL, Wu XM, Wang Y, Liu YJ, Luo H, Lv X, Gan YR, Song SD, Gao F. 2012. Complete genome sequence of *Acinetobacter baumannii* MDR-TJ and insights into its mechanism of antibiotic resistance. *J. Antimicrob. Chemother.* 67:2825–2832.
- Liou ML, Liu CC, Lu CW, Hsieh MF, Chang KC, Kuo HY, Lee CC, Chang CT, Yang CY, Tang CY. 2012. Genome sequence of *Acinetobacter baumannii* TYTH-1. *J. Bacteriol.* 194:6974.
- Smith MG, Gianoulis TA, Pukatzki S, Mekalanos JJ, Ornston LN, Gerstein M, Snyder M. 2007. New insights into *Acinetobacter baumannii* pathogenesis revealed by high-density pyrosequencing and transposon mutagenesis. *Genes Dev.* 21:601–614.
- Pasteran F, Alborno E, Faccone D, Gomez S, Valenzuela C, Morales M, Estrada P, Valenzuela L, Matheu J, Guerriero L, Arbizu E, Calderon Y, Ramon-Pardo P, Corso A. 2012. Emergence of NDM-1-producing *Klebsiella pneumoniae* in Guatemala. *J. Antimicrob. Chemother.* 67:1795–1797.
- Bonnin RA, Naas T, Poirel L, Nordmann P. 2012. Phenotypic, biochemical, and molecular techniques for detection of metallo-beta-lactamase NDM in *Acinetobacter baumannii*. *J. Clin. Microbiol.* 50:1419–1421.
- Siroi D, Siroi J, Labia R, Morand A, Courvalin P, Darfeuille-Michaud A, Perroux R, Cluzel R. 1987. Transferable resistance to third-generation cephalosporins in clinical isolates of *Klebsiella pneumoniae*: identification of CTX-1, a novel beta-lactamase. *J. Antimicrob. Chemother.* 20:323–334.